CLAIMS

We claim:

1. A method for quantitating a biological molecule in a sample with a mass spectrometer, comprising adding to the sample an internal standard substance that is a metabolically isotope labeled biological molecule, or a cell containing an internal standard substance that is a metabolically isotope labeled biological molecule.

2. A method for quantitating one or a plurality of biological molecules in a sample, comprising the steps of:

adding to the sample an internal standard substance that is a metabolically isotope labeled biological molecule, or a cell containing an internal standard substance that is a metabolically isotope labeled biological molecule, which are obtained by adding a precursor of a biological molecule that is isotope labeled, so as to culture;

extracting and fractionating a biological molecule from the each sample;

analyzing the each fractionated biological molecule with a mass spectroscopic device;

identifying the biological molecule from mass analysis information; and

determining a ratio of intensities between a labeled peak and an unlabeled peak of each biological molecule to quantitate the biological molecule.

3. The method according to Claim 1 or 2, wherein the ratio of peak intensity is compared between each sample to quantitate the biological molecule relatively.

4. The method according to any one of Claims 1 to 3, wherein the biological molecule in the internal standard substance that is the metabolically isotope labeled

biological molecule, or in the cell containing the internal standard substance that is the metabolically isotope labeled biological molecule, is present in a known quantity.

5. The method according to any one of Claims 1 to 4, wherein the quantitation is an absolute quantitation.

6. A method for quantitating one or a plurality of biological molecules in a sample, comprising the steps of:

(1) adding to a sample an internal standard substance that is a metabolically isotope labeled biological molecule, or a cell containing an internal standard substance that is a metabolically isotope labeled biological molecule;

(2) performing mass analysis of each biological molecule present in the sample;

(3) identifying the biological molecule from mass analysis information; and

(4) determining a ratio of intensities between a labeled peak and an unlabeled peak of each biological molecule to quantitate the biological molecule.

7. The method according to Claim 6, further comprising extracting and fractionating a biological molecule from the sample.

8. The method according to Claim 6 or 7, further comprising performing isotope labeling of the biological molecule metabolically by adding a precursor of the biological molecule that is isotope labeled so as to culture.

9. The method according to any one of Claims 6 to 8, wherein the method is performed for a plurality of samples, and further comprising comparing a ratio of peak

intensity of each biological molecule between each sample.

10.   The method according to any one of Claims 6 to 9, which is a method for quantitating one or a plurality of biological molecules in the sample absolutely,

5   wherein the biological molecule in the internal standard substance that is the metabolically isotope labeled biological molecule, or the biological molecule in the cell containing the internal standard substance that is the metabolically isotope labeled biological molecule, is present in a known quantity.

10   11.   The method according to any one of Claims 6 to 10, further comprising quantitating absolutely a biological molecule in the internal standard substance that is the metabolically isotope labeled biological molecule, or a biological molecule in the cell containing the internal standard substance that is the metabolically isotope labeled biological molecule.

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12.   The method according to Claim 11, wherein the step according to Claim 11 comprises the steps of:

(a)   adding a non-isotope labeled synthetic peptide to the internal standard substance that is the metabolically isotope labeled biological molecule, or to the cell

20   containing the internal standard substance that is the metabolically isotope labeled biological molecule;

(b)   extracting and fractionating a biological molecule from the internal standard substance that is the metabolically isotope labeled biological molecule or the cell containing the internal standard substance that is the metabolically isotope

25   labeled biological molecule;

(c)   performing mass analysis of the each fractionated biological molecule;

(d) identifying the biological molecule from mass analysis information; and

(e) determining a ratio of intensities between a labeled peak and an unlabeled peak of each biological molecule to quantitate absolutely the biological molecule.

5   13. The method according to any one of Claims 1 to 12, wherein the sample is a sample that is unable to be labeled metabolically.

14. The method according to any one of Claims 1 to 13, wherein the sample is a sample that is unable to be labeled by a cell culture.

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15. The method according to any one of Claims 1 to 14, wherein the biological molecule is a molecule selected from the group consisting of a protein, a lipid, a sugar chain, a nucleic acid, and combinations thereof.

15   16. The method according to any one of Claims 1 to 15, wherein the biological molecule is a protein.

17. The method according to any one of Claims 1 to 16, wherein the biological molecule is a protein, the method further comprises the steps of: extracting and

20   fractionating the protein; and digesting the protein.

18. The method according to any one of Claims 1 to 17, wherein the sample is a sample selected from the group consisting of a tissue, a biological fluid, a cell, a cell organ and a protein complex.

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19. The method according to any one of Claims 1 to 18, wherein the isotope is

an isotope selected from the group consisting of ^2H, ^{13}C, ^{15}N, ^{17}O, ^{18}O, ^{33}P, ^{34}S, and combinations thereof.

20.   The method according to any one of Claims 1 to 19, wherein the isotope is ^{13}C.

21.   An internal standard substance that is a metabolically isotope labeled biological molecule to be used in the method according to any one of Claims 1 to 20.

22.   A cell containing an internal standard substance that is a metabolically isotope labeled biological molecule to be used in the method according to any one of Claims 1 to 20.

23.   A reagent for use in the method according to any one of Claims 1 to 20, comprising an internal standard substance that is a metabolically isotope labeled biological molecule.

24.   A reagent for use in the method according to any one of Claims 1 to 20, comprising a cell containing an internal standard substance that is a metabolically isotope labeled biological molecule.

25.   A use of an internal standard substance that is a metabolically isotope labeled biological molecule for the method according to any one of Claims 1 to 20.

26.   A use of a cell containing an internal standard substance that is a metabolically isotope labeled biological molecule for the method according to any

one of Claims 1 to 20.

27. A program for causing a computer receiving data on mass analysis of one or a plurality of biological molecules in a sample obtained in a mass spectroscopic device to quantitate one or a plurality of biological molecules in the sample, the program comprising performing the steps of:

(1) receiving an analytical result obtained by analyzing with the mass spectroscopic device each biological molecule in the each sample, wherein an internal standard substance that is a metabolically isotope labeled biological molecule or a cell containing an internal standard substance that is a metabolically isotope labeled biological molecule is added to the sample;

(2) identifying the biological molecule from the analytical result of mass analysis; and

(3) determining a ratio of intensities between a labeled peak and an unlabeled peak of each biological molecule to quantitate the biological molecule.

28. A program for causing a computer receiving data on the mass analysis of one or a plurality of biological molecules in a sample obtained in a mass spectroscopic device to quantitate the one or a plurality of biological molecules in the sample, the program comprising performing the steps of:

(1) receiving an analytical result obtained by analyzing with the mass spectroscopic device each biological molecule in each sample, wherein an internal standard substance that is a metabolically isotope labeled biological molecule, or a cell containing an internal standard substance that is a metabolically isotope labeled biological molecule is added to the sample, and a biological molecule is extracted and fractionated from the each sample;

(2)   identifying the biological molecule from the analytical result of mass analysis; and

(3)   determining a ratio of intensities between a labeled peak and an unlabeled peak of each biological molecule to quantitate said biological molecule.

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29.   The program according to Claim 27 or 28, wherein analysis for a plurality of samples is performed, and further comprising performing of comparing a peak intensity ratio of each biological molecule between each sample.

10   30.   The program according to any one of Claims 27 to 29, which is a program for quantitating absolutely one or a plurality of biological molecules in the sample, and wherein the biological molecule in the internal standard substance that is the metabolically isotope labeled biological molecule, or in the cell containing the internal standard substance that is the metabolically isotope labeled biological molecule, is

15   present in a known quantity.

31.   An analysis system for analyzing data on mass analysis of a first biological molecule and a second biological molecule that has been isotope labeled with for corresponding to the first biological molecule, comprising:

20   a mass spectroscopic device for performing mass analysis of the first and the second biological molecules; and

a control unit comprising a data input and output unit for receiving the data on the mass analysis of the biological molecule from the mass spectroscopic device, wherein the control unit comprises:

25   a processing unit for determining a first m/z value of the first biological molecule for which a sequence of a biological molecular component has been determined, and

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a second m/z value of the second biological molecule for which a sequence of a

biological molecular component has been determined, and, extracting data

containing a mass spectrum against m/z values and a mass chromatogram of the

first biological molecule and the second biological molecule from data on mass

5   analysis obtained in the mass spectroscopic device, based on the first and the

second m/z values; and

a waveform processing unit for receiving the mass chromatogram at the first

and the second m/z values from the processing unit, and performing waveform

separation processing of the mass chromatogram against a time axis.

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32.   The analysis system according to Claim 31, wherein the determination of

the first and the second m/z values is carried out in such a way that the determination

of the second m/z value is made by determining from the first m/z value of the first

biological molecule for which the sequence of the biological molecular component

15   has been determined, based on information on the number of non-isotope labeled

component of the first biological molecule and an electric charge of the first biological

molecule, or the determination of the first m/z value is made by determining from the

second m/z value of the second biological molecule for which the sequence of the

biological molecular component has been determined, based on information on the

20   number of isotope labeled components of the second biological molecule and an

electric charge of the second biological molecule.

33.   The analysis system according to Claim 31 or 32, wherein the control unit

further comprises a computation unit for calculating an area of a waveform derived

25   from an individual biological molecule obtained by waveform separation processing

from the waveform separation processing unit, and calculating a ratio (an area of a

first waveform) / (an area of a second waveform) from a value of the area of the first

waveform derived from an individual biological molecule at the first m/z value and a

value of the area of the second waveform derived from an individual biological

molecule at the second m/z value.

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34. The analysis system according to any one of Claims 31 to 33, wherein the

control unit further comprises an information addition unit for performing, after

waveform separation, classification for each sequence of a component of the

biological molecule, retrieving the sequence with a database containing information

10   on the function of biological molecules, and linking the sequence to function from the

result of the verification so as to group.

35. The analysis system according to any one of Claims 31 to 34, wherein the

control unit further comprises a computation unit for identifying the biological

15   molecule from the sequence of the biological molecular component, and determining,

from a quantitative value of each biological molecular component constituting the

biological molecule, a mean value to serve as a representative quantitative value for

the biological molecule.

20   36. The analysis system according to any one of Claims 31 to 35, wherein the

control unit further comprises an information addition unit for retrieving the sequence

of the biological molecular component with the database containing information on

the function of biological molecules, and acquiring information on function of the

biological molecule.

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37. The analysis system according to any one of Claims 31 to 36, wherein

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when mass analyses of the first and the second biological molecules are performed in the presence of an internal standard substance,

the waveform processing unit for receiving a mass chromatogram at the m/z value of the internal standard substance and further performing waveform separation

5   processing to obtain a waveform specific to the internal standard substance, and

the computation unit for calculating an area of the waveform specific to the internal standard substance from the waveform processing unit and at the same time further calculating a ratio (the area of the first waveform) / (the area of the waveform specific to the internal standard substance), and/or a ratio (the area of the second

10   waveform) / (the area of the waveform specific to the internal standard substance).

38.   An analysis system for analyzing data on mass analysis of an internal standard substance, which is an isotope labeled biological molecule for corresponding to a first and a second biological molecule, comprising:

15   a mass spectroscopic device for performing mass analysis of the first and the second biological molecules as well as the isotope labeled biological molecule; and

a control unit comprising a data input and output unit for receiving the data on mass analysis of the biological molecules from the mass spectroscopic device;

wherein the control unit comprises:

20   a processing unit for determining a first m/z value and a second m/z value of the biological molecule for which a sequence of a biological molecular component has been determined and a m/z value of an internal standard substance which is isotope labeled biological molecule for which a sequence of a biological molecular component has been determined, and, extracting data containing mass spectrum

25   against the m/z value and a mass chromatogram of the first and the second biological molecules as well as of the biological molecule constituting the internal

standard substance from the data on mass analysis obtained in the mass spectroscopic device, based on the m/z values of the first and the second as well as the internal standard substance; and

a waveform processing unit for receiving the mass chromatogram at the m/z

5   values of the first and the second biological molecules as well as the internal standard substance from the processing unit and performing waveform separation processing of the mass chromatogram.

39.   The analysis system according to Claim 38, wherein the determination of

10   the first m/z value and the second m/z value, as well as the m/z value of the internal standard substance is carried out in such a way that the determination of the m/z value of the biological molecule constituting the internal standard substance is made by determining, from the first m/z value and the second m/z value of the first and the second biological molecules for which a sequence of the biological molecular

15   component has been determined, based on information on the number of non-isotope labeled components of the first and the second biological molecules and an electric charge of the first and the second biological molecules, or the determination of the first m/z value and the second m/z value of the first and the second biological molecules is made by determining, from the m/z value of the internal standard

20   substance for which a sequence of the biological molecular component has been determined, based on information on the number of isotope labeled biological molecular components of the internal standard substance and an electric charge of the biological molecule constituting the internal standard substance.

25   40.   The analysis system according to Claim 38 or 39, wherein the control unit further comprises a computation unit for calculating an area of a waveform derived

from an individual biological molecule obtained by waveform separation processing

from the waveform separation processing unit, and calculating a ratio (an area of a

first waveform) / (an area of a waveform specific to the internal standard substance),

and/or, a ratio (an area of a second waveform) / (an area of a waveform specific to

5   the internal standard substance) from values of the areas of the first waveform and

the second waveform derived from specific biological molecules at the first and the

second m/z values, and a value of the area of the internal standard substance

waveform derived from an individual biological molecule at the m/z value of the

internal standard substance.

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41.   The analysis system according to any one of Claims 38 to 40, wherein the

control unit further comprises an information addition unit for performing, after

waveform separation, classification for each sequence of the biological molecular

component, retrieving the sequence with a database containing information on the

15   function of biological molecules, and linking the sequence with function from the

result of the verification so as to group.

42.   The analysis system according to any one of Claims 38 to 41, wherein the

control unit further comprises a computation unit for identifying the biological

20   molecule from the sequence of the biological molecular component, and determining,

from a quantitative value of each biological molecular component constituting the

biological molecule, a mean value to serve as a representative quantitative value for

the biological molecule.

25   43.   The analysis system according to any one of Claims 38 to Claim 42,

wherein the control unit further comprises an information addition unit for retrieving

the sequence of the biological molecular component with the database containing

information on the function of biological molecules, and acquiring information on

function of the biological molecule.

5   44.   The analysis system according to any one of Claims 31 to 43, wherein the

isotope used in the isotope labeling is any isotope selected from the group consisting

of ^{2}H, ^{13}C, ^{15}N, ^{17}O, ^{18}O, ^{33}P and ^{34}S, as well as combinations thereof.

45.   The analysis system according to any one of Claims 31 to 44, wherein the

10   determination of the sequence of the component is carried out by MS / MS

processing.

46.   The analysis system according to Claim 45, wherein the determination of

the sequence of the component is carried out by retrieving data obtained by MS / MS

15   processing with a database regarding a biological molecule.

47.   The analysis system according to any one of Claims 31 to 46, wherein the

biological molecule is a biological molecule that has been separated from the sample

over time.

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48.   The analysis system according to any one of Claims 31 to 47, wherein the

biological molecule is any molecule selected from the group consisting of a protein, a

lipid, a sugar chain and a nucleic acid, as well as combinations thereof.

25   49.   An analysis method for analyzing data on mass analysis of a first

biological molecule and a second biological molecule that has been isotope labeled

for corresponding to the first biological molecule, comprising the steps of:

determining, among the data on the mass analysis of the biological molecule measured in a mass spectroscopic device, a first m/z value of the first biological molecule for which a sequence of a biological molecular component has been

5   determined, and a second m/z value of the second biological molecule for which a sequence of a biological molecular component has been determined,

extracting data containing a mass spectrum against m/z values and a mass chromatogram of the first biological molecule and the second biological molecule from the data on the mass analysis, based on the first and the second m/z values;

10   and

performing waveform separation processing of the mass chromatogram of the first and the second biological molecules.

50.   The analysis method according to Claim 49, wherein the determination of

15   the first m/z value and the second m/z value is carried out in such a way that the determination of the second m/z value is made by determining from the first m/z value of the first biological molecule for which the sequence of the biological molecular component has been determined, based on information on the number of non-isotope labeled components of the first biological molecule and an electric

20   charge of the first biological molecule, or the determination of the first m/z value of the second biological molecule is made by determining from the second m/z value of the second biological molecule for which the sequence of the biological molecular component has been determined, based on information on the number of isotope labeled components of the second biological molecule and an electric charge of the

25   second biological molecule.

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51. The analysis method according to Claim 49 or Claim 50, further comprising the steps of:

calculating an area of a waveform derived from an individual biological molecule obtained by the waveform separation processing step; and

5   calculating a ratio (an area of a first waveform) / (an area of a second waveform) from a value of the area of the first waveform derived from an individual biological molecule at the first m/z value, and a value of the area of the second waveform derived from an individual biological molecule at the second m/z value.

10   52. The analysis method according to any one of Claims 49 to 51, further comprising the steps of:

performing, after the waveform separation, classification for each sequence of a component of the biological molecule,

retrieving the sequence with a database containing information on the function

15   of biological molecules, and

linking the sequence to function from the result of the verification so as to group.

53. The analysis method according to any one of Claims 49 to 52, further comprising the steps of:

20   identifying the biological molecule from the sequence of the biological molecular component; and

determining, from a quantitative value of each biological molecular component constituting the biological molecule, a mean value to serve as a representative quantitative value for the biological molecule.

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54. The analysis method according to any one of Claims 49 to 53, further

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comprising retrieving the sequence of the biological molecular component with a database containing information on the function of biological molecules so as to acquire information on the function of the biological molecule.

5   55. The analysis method according to any one of Claims 49 to 54, further comprising the steps of:

performing determination of a m/z value of the internal standard substance along with m/z values of the first and the second biological molecules, extraction of data containing a mass chromatogram of the internal standard substance, waveform

10   separation processing of the mass chromatogram of the internal standard substance and calculation of an area of a waveform specific to the internal standard substance; and

calculating a ratio (the area of the first waveform) / (the area of the waveform specific to the internal standard substance), and/or, a ratio (the area of the second

15   waveform) / (the area of the waveform specific to the internal standard substance).

56. An analysis method for analyzing data on mass analysis of an internal standard substance, which is a biological molecule that has been isotope labeled for corresponding to a first and a second biological molecule, comprising the steps of:

20   determining, among the data on the mass analysis of the biological molecules measured in a mass spectroscopic device, a first m/z value and a second m/z value of the first and the second biological molecules for which a sequence of a biological molecular component has been determined, and a m/z value of the biological molecule constituting the internal standard substance for which a sequence of a

25   biological molecular component has been determined;

extracting data containing a mass spectrum against m/z values and a mass

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chromatogram of the first and the second biological molecules as well as of the biological molecule constituting the internal standard substance from the data on the mass analysis, based on the m/z values of the first and the second as well as of the internal standard substance; and

5   performing waveform separation processing on the mass chromatogram of the first and second of the biological molecules, as well as the biological molecule constituting the internal standard substance.

57.   The analysis method according to Claim 56, wherein the determination of
10 the first m/z value and the second m/z value, as well as the m/z value of the internal standard substance is carried out in such was that the determination of the m/z value of the biological molecule constituting the internal standard substance is made by determining, from the first m/z value and the second m/z value of the first and the second biological molecules for which a sequence of the biological molecular
15 component has been determined, based on information on the number of non-isotope labeled components of the first and the second biological molecules and an electric charge of the first and the second biological molecules, or the determination of the first m/z value and the second m/z value is made by determining, from the m/z value of the internal standard substance for which a sequence of the biological
20 molecular component has been determined, based on information on the number of isotope labeled biological molecular components of the internal standard substance and an electric charge of the biological molecule constituting the internal standard substance.

25   58.   The analysis method according to Claim 56 or 57, further comprising the steps of:

calculating an area of a waveform derived from an individual biological

molecule obtained by the waveform separation processing step; and

performing calculation a ratio (an area of a first waveform) / (an area of a

waveform specific to the internal standard substance), and/or, a ratio (an area of a

5   second waveform) / (an area of a waveform specific to the internal standard

substance) from values of the areas of the first and the second waveforms derived

from specific biological molecules at the first and the second m/z values, and a value

of the area of the internal standard substance waveform derived from an individual

biological molecule at m/z value of the internal standard substance.

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59.   The analysis method according to any one of Claims 56 to 58, further

comprising the steps of:

performing, after the waveform separation, classification for each sequence of

the component of the biological molecule;

15   retrieving the sequence with a database containing information on the function

of biological molecules; and

linking the sequence to function from the result of the verification so as to group.

60.   The analysis method according to any one of Claims 56 to 59, further

20   comprising the steps of:

identifying the biological molecule from the sequence of the biological molecular

component; and

determining, from a quantitative value of each biological molecular component

constituting the biological molecule, a mean value to serve as a representative

25   quantitative value for the biological molecule.

61. The analysis method according to any one of Claims 56 to 60, further comprising retrieving the sequence of the biological molecular component with a database containing information on the function of biological molecules so as to acquire information on the function of the biological molecule.

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62. The analysis method according to any one of Claims 49 to 61, wherein the isotope used in the isotope labeling is any isotope selected from the group consisting of ^2H, ^{13}C, ^{15}N, ^{17}O, ^{18}O, ^{33}P and ^{34}S, as well as combinations thereof.

10 63. The analysis method according to any one of Claims 49 to 62, wherein the determination of the sequence of the component is carried out by MS / MS processing.

64. The analysis method according to Claim 63, wherein the determination of 15 the sequence of the component is carried out by retrieving data obtained by MS / MS processing with a database regarding a biological molecule.

65. The analysis method according to any one of Claims 49 to 64, wherein the biological molecule is a biological molecule that has been separated from the sample 20 over time.

66. The analysis method according to any one of Claims 49 to 65, wherein the biological molecule is any molecule selected from the group consisting of a protein, a lipid, a sugar chain and a nucleic acid, as well as combinations thereof.

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67. A program for causing a computer receiving data obtained in a mass

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spectroscopic device to analyze the data in which the data is related to mass analysis of a first biological molecule and a second biological molecule, which has been isotope labeled for corresponding to the first biological molecule, the program performing the steps of:

5   determining, among the data on the mass analysis of the biological molecule measured in the mass spectroscopic device, a first m/z value of the first biological molecule for which a sequence of a biological molecular component has been determined, and a second m/z value of the second biological molecule for which a sequence of a biological molecular component has been determined,

10   extracting data containing a mass spectrum against m/z values and a mass chromatogram of the first biological molecule and the second biological molecule from the data on the mass analysis, based on the first and the second m/z values; and

performing waveform separation processing of the mass chromatogram of the

15   first and the second biological molecules.

68.   The program according to Claim 67, wherein the determination of the first m/z value and the second m/z value is carried out in such a way that the determination of the second m/z value is made by determining from the first m/z

20   value of the first biological molecule for which the sequence of the biological molecular component has been determined, based on information on the number of non-isotope labeled components of the first biological molecule and an electric charge of the first biological molecule, or the determination of the first m/z value of the second biological molecule is made by determining from the second m/z value of

25   the second biological molecule for which the sequence of the biological molecular component has been determined, based on information on the number of isotope

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labeled components of the second biological molecule and an electric charge of the second biological molecule.

69. The program according to Claim 67 or 68, further comprising performing

5 the steps of:

calculating an area of a waveform derived from an individual biological molecule obtained by the waveform separation processing step; and

calculating a ratio (an area of a first waveform) / (an area of a second waveform) from a value of the area of the first waveform derived from an individual

10 biological molecule at the first m/z value, and a value of the area of the second waveform derived from an individual biological molecule at the second m/z value.

70. The program according to any one of Claims 67 to 69, further comprising performing the steps of:

15 performing, after the waveform separation, classification for each sequence of a component of the biological molecule,

retrieving the sequence with a database containing information on the function of biological molecules, and

linking the sequence to function from the result of the verification so as to group.

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71. The program according to any one of Claims 67 to 70, further comprising performing the steps of:

identifying the biological molecule from the sequence of the biological molecular component; and

25 determining, from a quantitative value of each biological molecular component constituting the biological molecule, a mean value to serve as a representative

quantitative value for the biological molecule.

72.   The program according to any one of Claims 67 to 71, further comprising

performing of retrieving the sequence of the biological molecular component with a

5   database containing information on the function of biological molecules so as to

acquire information on the function of the biological molecule.

73.   The program according to any one of Claims 67 to 72, further comprising

performing the steps of:

10   obtaining, in the mass spectroscopic device, data on the mass analysis of an

internal standard substance along with the mass analysis of the first and the second

biological molecules,

extracting a mass chromatogram of the internal standard substance from the

data on the mass analysis, and performing waveform separation processing of the

15   mass chromatogram of the internal standard substance, and

calculating an area of a waveform specific to the internal standard substance

obtained from the waveform separation processing to compute a ratio (an area of a

first waveform) / (an area of a waveform specific to the internal standard substance),

and/or, a ratio (an area of a second waveform) / (an area of a waveform specific to

20   the internal standard substance).

74.   A program for causing a computer receiving data obtained in a mass

spectroscopic device to analyze the data in which the data is related to mass

analysis of a first and a second biological molecule, and an internal standard

25   substance, which is a biological molecule that has been isotope labeled for

corresponding to the first and the second biological molecules, the program

performing the steps of:

determining, among the data on the mass analysis of the biological molecules measured in the mass spectroscopic device, a first m/z value and a second m/z value of the first and the second biological molecules for which a sequence of a

5   biological molecular component has been determined, and a m/z value of the biological molecule constituting the internal standard substance for which a sequence of a biological molecular component has been determined;

extracting data containing a mass spectrum against m/z values and a mass chromatogram of the first and the second biological molecules as well as of the

10   internal standard substance biological molecule from the data on the mass analysis, based on the m/z values of the first and the second as well as of the internal standard substance; and

performing waveform separation processing of the mass chromatogram of the first and second of the biological molecules, as well as the biological molecule

15   constituting the internal standard substance.

75.   The program according to Claim 74, wherein the determination of the first m/z value and the second m/z value, as well as the m/z value of the internal standard substance is carried out in such was that the determination of the m/z value of the

20   biological molecule constituting the internal standard substance is made by determining, from the first m/z value and the second m/z value of the first and the second biological molecules for which a sequence of the biological molecular component has been determined, based on information on the number of non-isotope labeled components of the first and the second biological molecules and an

25   electric charge of the first and the second biological molecules, or the determination of the first m/z value and the second m/z value is made by determining, from the m/z

value of the internal standard substance for which a sequence of the biological

molecular component has been determined, based on information on the number of

isotope labeled biological molecular components of the internal standard substance

and an electric charge of the biological molecule constituting the internal standard

5   substance.

76.   The program according to Claim 74 or 75, further comprising performing

the steps of:

calculating an area of a waveform derived from an individual biological molecule

10   obtained by the waveform separation processing step; and

performing calculation a ratio (an area of a first waveform) / (an area of a

waveform specific to the internal standard substance), and/or, a ratio (an area of a

second waveform) / (an area of a waveform specific to the internal standard

substance) from values of the areas of the first and the second waveforms derived

15   from specific biological molecules at the first and the second m/z values, and a value

of the area of the internal standard substance waveform derived from an individual

biological molecule at m/z value of the internal standard substance.

77.   The program according to any one of Claims 74 to 76, further comprising

20   performing the steps of:

performing, after the waveform separation, classification for each sequence of

the component of the biological molecule;

retrieving the sequence with a database containing information on the function

of biological molecules; and

25   linking the sequence to function from the result of the verification so as to group.

78. The program according to any one of Claims 74 to 77, further comprising performing the steps of:

identifying the biological molecule from the sequence of the biological molecular component; and

5   determining, from a quantitative value of each biological molecular component constituting the biological molecule, a mean value to serve as a representative quantitative value for the biological molecule.

79. The program according to any one of Claims 74 to 78, further comprising

10   performing of retrieving the sequence of the biological molecular component with a database containing information on the function of biological molecules so as to acquire information on the function of the biological molecule.

80. The program according to any one of Claims 67 to 79, wherein the isotope

15   used in the isotope labeling is any isotope selected from the group consisting of ^{2}H, ^{13}C, ^{15}N, ^{17}O, ^{18}O, ^{33}P and ^{34}S, as well as combinations thereof.

81. The program according to any one of Claims 67 to 80, wherein the determination of the sequence of the component is carried out by MS / MS

20   processing.

82. The program according to Claim 81, wherein the determination of the sequence of the component is carried out by retrieving data obtained by MS / MS processing with a database regarding the biological molecule.

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83. The program according to any one of Claims 67 to 82, wherein the

biological molecule is a biological molecule that has been separated from the sample over time.

84.   The program according to any one of Claims 67 to 83, wherein the
5   biological molecule is any molecule selected from the group consisting of a protein, a lipid, a sugar chain and a nucleic acid, as well as combinations thereof.

85.   An analysis method for analyzing data on mass analysis of an internal standard substance, which is a biological molecule that has been isotope labeled for
10   corresponding to a first and a second biological molecule, comprising the steps of:
        determining, among data on the mass analysis of the biological molecule measured in a mass spectroscopic device, a first m/z value and a second m/z value of the first and the second biological molecules for which a sequence of a biological molecular component has been determined, and a m/z value of a biological molecule
15   constituting an internal standard substance for which a sequence of a biological molecular component has been determined; and
        retrieving with a database containing information on the function of biological molecules based on the obtained data, so as to acquire information on the function of the biological molecule.

20

86.   The analysis method, further comprising, after the determination step, extracting a mass spectrum against m/z values and a mass chromatogram of the first and the second biological molecules as well as of the biological molecule constituting the internal standard substance, from the data on the mass analysis, based on the
25   first and the second m/z values as well as the m/z value of the internal standard substance.

87. The analysis method according to Claim 85 or 86, wherein the

determination of the first m/z value and the second m/z value, as well as the m/z

value of the internal standard substance is carried out in such was that the

5   determination of the m/z value of the biological molecule constituting the internal

standard substance is made by determining, from the first m/z value and the second

m/z value of the first and the second biological molecules for which a sequence of

the biological molecular component has been determined, based on information on

the number of non-isotope labeled components of the first and the second biological

10   molecules and an electric charge of the first and the second biological molecules, or

the determination of the first m/z value and the second m/z value is made by

determining, from the m/z value of the internal standard substance for which a

sequence of the biological molecular component has been determined, based on

information on the number of isotope labeled biological molecular components of the

15   internal standard substance and an electric charge of the biological molecule

constituting the internal standard substance.

88. The analysis method according to any one of Claims 85 to 87, further

comprising performing calculation of a ratio (a first peak) / (a peak specific to the

20   internal standard substance), and/or, a ratio (a second peak) / (a peak specific to the

internal standard substance) from values of the first and the second peaks derived

from specific biological molecules at the first and the second m/z values, and a value

of an internal standard substance peak derived from an individual biological molecule

at the m/z value of the internal standard substance.

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89. The analysis method according to any one of Claims 85 to 88, further

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comprising linking the sequence to function from the result of the verification so as to group.

90. The analysis method according to any one of Claims 85 to 89, further

5 comprising the steps pf:

identifying the biological molecule from the sequence of the biological molecular component; and

determining, from a quantitative value of each biological molecular component constituting the biological molecule, a mean value to serve as a representative

10 quantitative value for the biological molecule.

91. The analysis method according to any one of Claims 85 to 90, wherein the isotope used in the isotope labeling is any isotope selected from the group consisting of ^{2}H, ^{13}C, ^{15}N, ^{17}O, ^{18}O, ^{33}P and ^{34}S, as well as combinations thereof.

15

92. The analysis method according to any one of Claims 85 to 91, wherein the determination of the sequence of the component is carried out by MS / MS processing.

20 93. The analysis method according to Claim 92, wherein the determination of the sequence of the component is carried out by retrieving data obtained by MS / MS processing with a database regarding a biological molecule.

94. The analysis method according to any one of Claims 85 to 93, wherein the

25 biological molecule is a biological molecule that has been separated from the sample over time.

95. The analysis method according to any one of Claims 85 to 94, wherein the biological molecule is any molecule selected from the group consisting of a protein, a lipid, a sugar chain, and a nucleic acid, as well as combinations thereof.

5

96. A program for causing a computer receiving data obtained in a mass spectroscopic device to analyze the data in which the data is related to mass analysis of a first and a second biological molecule, and an internal standard substance, which is a biological molecule that has been isotope labeled for

10 corresponding to the first and the second biological molecules, the program performing the steps of:

determining, among the data on the mass analysis of the biological molecule measured in the mass spectroscopic device, a first m/z value and second m/z value of the first and the second biological molecules for which a sequence of a biological

15 molecular component has been determined, and a m/z value of a biological molecule constituting an internal standard substance for which a sequence of a biological molecular component has been determined,

retrieving with a database containing information on the function of biological molecules based on the obtained data, so as to acquire information on the function of

20 the biological molecule.

97. The program according to Claim 96, further comprising performing of, after the determination step, extracting a mass spectrum against m/z values and a mass chromatogram of the first and the second biological molecules as well as of the

25 biological molecule constituting the internal standard substance, from the data on the mass analysis, based on the first and the second m/z values as well as the m/z value

of the internal standard substance.

98. The program according to Claim 96 or 97, wherein the determination of the first m/z value and the second m/z value, as well as the m/z value of the internal

5 standard substance is carried out in such was that the determination of the m/z value of the biological molecule constituting the internal standard substance is made by determining, from the first m/z value and the second m/z value of the first and the second biological molecules for which a sequence of the biological molecular component has been determined, based on information on the number of non-

10 isotope labeled components of the first and the second biological molecules and an electric charge of the first and the second biological molecules, or the determination of the first m/z value and the second m/z value is made by determining, from the m/z value of the internal standard substance for which a sequence of the biological molecular component has been determined, based on information on the number of

15 isotope labeled biological molecular components of the internal standard substance and an electric charge of the biological molecule constituting the internal standard substance.

99. The program according to any one of Claims 96 to 98, further comprising

20 performing calculation of a ratio (a first peak) / (a peak specific to the internal standard substance), and/or, a ratio (a second peak) / (a peak specific to the internal standard substance) from values of the first and the second peaks derived from specific biological molecules at the first and the second m/z values, and a value of an internal standard substance peak derived from an individual biological molecule at

25 the m/z value of the internal standard substance.

100. The program according to any one of Claims 96 to 99, further comprising performing of linking the sequence to function from the result of the verification so as to group.

5   101. The program according to any one of Claims 96 to 100, further comprising performing the steps pf:

identifying the biological molecule from the sequence of the biological molecular component; and

determining, from a quantitative value of each biological molecular component

10   constituting the biological molecule, a mean value to serve as a representative quantitative value for the biological molecule.

102. The program according to any one of Claims 96 to 101, wherein the isotope used in the isotope labeling is any isotope selected from the group

15   comprising ^{2}H, ^{13}C, ^{15}N, ^{17}O, ^{18}O, ^{33}P and ^{34}S, as well as combinations thereof.

103. The program according to any one of Claims 96 to 102, wherein the determination of the sequence of the component is carried out by MS / MS processing.

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104. The program according to Claim 103, wherein the determination of the sequence of the component is carried out by retrieving data obtained by MS / MS processing with a database regarding a biological molecule.

25   105. The program according to any one of Claims 96 to 104, wherein the biological molecule is a biological molecule that has been separated from the sample

over time.

106. The program according to any one of Claims 96 to 105, wherein the biological molecule is any molecule selected from the group consisting of a protein, a

5 lipid, a sugar chain and a nucleic acid, as well as combinations thereof.

107. A program for causing a computer receiving data on mass analysis obtained in a mass spectroscopic device in which the date is related to one or a plurality of biological molecules in a sample, to quantitate the one or a plurality of

10 biological molecules in the sample, the program performing the steps of:

determining, among the data on the mass analysis of the biological molecule measured in the mass spectroscopic device, a first m/z value of the first biological molecule for which a sequence of a biological molecular component has been determined, and a second m/z value of the second biological molecule for which a

15 sequence of a biological molecular component has been determined,

extracting data containing a mass spectrum against m/z values and a mass chromatogram of the first biological molecule and the second biological molecule from the data on the mass analysis, based on the first and the second m/z values; and

20 performing waveform separation processing of the mass chromatogram of the first and the second biological molecules.

108. The program according to Claim 107, wherein the determination of the first m/z value and the second m/z value is carried out in such a way that the

25 determination of the second m/z value is made by determining from the first m/z value of the first biological molecule for which the sequence of the biological

molecular component has been determined, based on information on the number of

non-isotope labeled components of the first biological molecule and an electric

charge of the first biological molecule, or the determination of the first m/z value of

the second biological molecule is made by determining from the second m/z value of

5　the second biological molecule for which the sequence of the biological molecular

component has been determined, based on information on the number of isotope

labeled components of the second biological molecule and an electric charge of the

second biological molecule.

10　109.　The program according to Claim 107 or 108, further comprising

performing the steps of:

　　calculating an area of a waveform derived from an individual biological molecule

obtained by the waveform separation processing step; and

　　calculating a ratio (an area of a first waveform) / (an area of a second

15　waveform) from a value of the area of the first waveform derived from an individual

biological molecule at the first m/z value, and a value of the area of the second

waveform derived from an individual biological molecule at the second m/z value.

　　110.　The program according to any one of Claims 107 to 109, further

20　comprising performing the steps of:

　　performing, after the waveform separation, classification for each sequence of a

component of the biological molecule,

　　retrieving the sequence with a database containing information on the function

of biological molecules, and

25　　linking the sequence to function from the result of the verification so as to group.

111.   The program according to any one of Claims 107 to 110, further comprising performing the steps of:

identifying the biological molecule from the sequence of the biological molecular component; and

5   determining, from a quantitative value of each biological molecular component constituting the biological molecule, a mean value to serve as a representative quantitative value for the biological molecule.

112. The program according to any one of Claims 107 to 111, further

10   comprising performing of retrieving the sequence of the biological molecular component with a database containing information on the function of biological molecules so as to acquire information on the function of the biological molecule.

113. The program according to any one of Claims 107 to 112, wherein the

15   isotope used in the isotope labeling is any isotope selected from the group comprising ^{2}H, ^{13}C, ^{15}N, ^{17}O, ^{18}O, ^{33}P and ^{34}S, as well as combinations thereof.

114. The program according to any one of Claims 107 to 113, wherein the determination of the sequence of the component is carried out by MS / MS

20   processing.

115. The program according to Claim 114, wherein the determination of the sequence of the component is carried out by retrieving data obtained by MS / MS processing with a database regarding a biological molecule.

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116. The program according to any one of Claims 107 to 115, wherein the

biological molecule is a biological molecule that has been separated from the sample over time.

117. The program according to any one of Claims 107 to 116, wherein the biological molecule is any molecule selected from the group consisting of a protein, a lipid, a sugar chain and a nucleic acid, as well as combinations thereof.